

SEQUENCE LISTING

<110> Svendsen, Allan
Draborg, Henriette

<120> Subtilase variants

<130> 10203

<160> 24

<170> PatentIn version 3.2

<210> 1

<211> 311

<212> PRT

<213> TY145 subtilase

<220>

<221> PEPTIDE

<222> (1)..(311)

<400> 1

Ala Val Pro Ser Thr Gln Thr Pro Trp Gly Ile Lys Ser Ile Tyr Asn
1 5 10 15

Asp Gln Ser Ile Thr Lys Thr Thr Gly Gly Ser Gly Ile Lys Val Ala
20 25 30

Val Leu Asp Thr Gly Val Tyr Thr Ser His Leu Asp Leu Ala Gly Ser
35 40 45

Ala Glu Gln Cys Lys Asp Phe Thr Gln Ser Asn Pro Leu Val Asp Gly
50 55 60

Ser Cys Thr Asp Arg Gln Gly His Gly Thr His Val Ala Gly Thr Val
65 70 75 80

Leu Ala His Gly Gly Ser Asn Gly Gln Gly Val Tyr Gly Val Ala Pro
85 90 95

Gln Ala Lys Leu Trp Ala Tyr Lys Val Leu Gly Asp Asn Gly Ser Gly
100 105 110

Tyr Ser Asp Asp Ile Ala Ala Ile Arg His Val Ala Asp Glu Ala
115 120 125

Ser Arg Thr Gly Ser Lys Val Val Ile Asn Met Ser Leu Gly Ser Ser
130 135 140

Ala Lys Asp Ser Leu Ile Ala Ser Ala Val Asp Tyr Ala Tyr Gly Lys
145 150 155 160

Gly Val Leu Ile Val Ala Ala Ala Gly Asn Ser Gly Ser Gly Ser Asn
165 170 175

Thr Ile Gly Phe Pro Gly Gly Leu Val Asn Ala Val Ala Val Ala Ala
180 185 190

Leu Glu Asn Val Gln Gln Asn Gly Thr Tyr Arg Val Ala Asp Phe Ser
195 200 205

Ser Arg Gly Asn Pro Ala Thr Ala Gly Asp Tyr Ile Ile Gln Glu Arg
210 215 220

Asp Ile Glu Val Ser Ala Pro Gly Ala Ser Val Glu Ser Thr Trp Tyr
225 230 235 240

Thr Gly Gly Tyr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His
245 250 255

Val Ala Gly Leu Ala Ala Lys Ile Trp Ser Ala Asn Thr Ser Leu Ser
260 265 270

His Ser Gln Leu Arg Thr Glu Leu Gln Asn Arg Ala Lys Val Tyr Asp
275 280 285

Ile Lys Gly Gly Ile Gly Ala Gly Thr Gly Asp Asp Tyr Ala Ser Gly
290 295 300

Phe Gly Tyr Pro Arg Val Lys
305 310

<210> 2
<211> 420
<212> PRT
<213> TA39 subtilase

<220>
<221> PEPTIDE
<222> (1)..(420)

<400> 2

Met Lys Arg Ser Gly Lys Ile Phe Thr Thr Ala Met Leu Ala Val Thr
1 5 10 15

Leu Met Met Pro Ala Met Gly Val Ser Ala Asn Glu Gly Asn Ala Ala
20 25 30

Ala Glu Gly Asn Glu Lys Phe Arg Val Leu Val Asp Ser Val Asp Gln
35 40 45

Lys Asn Leu Lys Asn Ala Lys Gln Gln Tyr Gly Val His Trp Asp Phe
50 55 60

Ala Gly Glu Gly Phe Thr Thr Asp Met Asn Glu Lys Gln Phe Asn Ala
65 70 75 80

Leu Lys Lys Asn Lys Asn Leu Thr Val Glu Lys Val Pro Glu Leu Glu
85 90 95

Ile Ala Thr Ala Thr Asp Lys Pro Glu Ala Leu Tyr Asn Ala Met Ala
100 105 110

Ala Ser Gln Ser Thr Pro Trp Gly Ile Lys Ala Ile Tyr Asn Asn Ser
115 120 125

Ser Ile Thr Gln Thr Ser Gly Gly Gly Ile Asn Ile Ala Val Leu
130 135 140

Asp Thr Gly Val Asn Thr Asn His Pro Asp Leu Arg Asn Asn Val Glu
145 150 155 160

Gln Cys Lys Asp Phe Thr Val Gly Thr Thr Tyr Thr Asn Asn Ser Cys
165 170 175

Thr Asp Arg Gln Gly His Gly Thr His Val Ala Gly Ser Ala Leu Ala
180 185 190

Asp Gly Gly Thr Gly Asn Gly Val Tyr Gly Val Ala Pro Asp Ala Asp
195 200 205

Leu Trp Ala Tyr Lys Val Leu Gly Asp Asp Gly Ser Gly Tyr Ala Asp
210 215 220

Asp Ile Ala Ala Ala Ile Arg His Ala Gly Asp Gln Ala Thr Ala Leu
225 230 235 240

Asn Thr Lys Val Val Ile Asn Met Ser Leu Gly Ser Ser Gly Glu Ser
245 250 255

Ser Leu Ile Thr Asn Ala Val Asn Tyr Ser Tyr Asn Lys Gly Val Leu
260 265 270

Ile Ile Ala Ala Ala Gly Asn Ser Gly Pro Tyr Gln Gly Ser Ile Gly
275 280 285

Tyr Pro Gly Ala Leu Val Asn Ala Val Ala Val Ala Ala Leu Glu Asn
290 295 300

Lys Val Glu Asn Gly Thr Tyr Arg Val Ala Asp Phe Ser Ser Arg Gly
305 310 315 320

Tyr Ser Trp Thr Asp Gly Asp Tyr Ala Ile Gln Lys Gly Asp Val Glu
325 330 335

Ile Ser Ala Pro Gly Ala Ala Ile Tyr Ser Thr Trp Phe Asp Gly Gly
340 345 350

Tyr Ala Thr Ile Ser Gly Thr Ser Met Ala Ser Pro His Ala Ala Gly
355 360 365

Leu Ala Ala Lys Ile Trp Ala Gln Tyr Pro Ser Ala Ser Asn Val Asp
370 375 380

Val Arg Gly Glu Leu Gln Tyr Arg Ala Tyr Glu Asn Asp Ile Leu Ser
385 390 395 400

Gly Tyr Tyr Ala Gly Tyr Gly Asp Asp Phe Ala Ser Gly Phe Gly Phe
405 410 415

Ala Thr Val Gln
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<210> 3
<211> 419
<212> PRT

<213> TA41 subtilase

<220>

<221> PEPTIDE

<222> (1)..(419)

<400> 3

Met Lys Arg Ser Gly Lys Ile Phe Thr Thr Ala Met Leu Ala Val Thr
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Leu Met Met Pro Ala Ile Gly Val Ser Ala Asn Arg Gly Asn Ala Ala
20 25 30

Asp Gly Asn Glu Lys Phe Arg Val Leu Val Asp Ser Ala Asn Gln Asn
35 40 45

Asn Leu Lys Asn Val Lys Glu Gln Tyr Gly Val His Trp Asp Phe Ala
50 55 60

Gly Glu Gly Phe Thr Thr Asn Met Asn Glu Lys Gln Phe Asn Ala Leu
65 70 75 80

Gln Asn Asn Lys Asn Leu Thr Val Glu Lys Val Pro Glu Leu Glu Ile
85 90 95

Ala Thr Ala Thr Asn Lys Pro Glu Ala Leu Tyr Asn Ala Met Ala Ala
100 105 110

Ser Gln Ser Thr Pro Trp Gly Ile Lys Ala Ile Tyr Asn Asn Ser Asn
115 120 125

Leu Thr Ser Thr Ser Gly Gly Ala Gly Ile Asn Ile Ala Val Leu Asp
130 135 140

Thr Gly Val Asn Thr Asn His Pro Asp Leu Ser Asn Asn Val Glu Gln
145 150 155 160

Cys Lys Asp Phe Thr Val Gly Thr Asn Phe Thr Asp Asn Ser Cys Thr
165 170 175

Asp Arg Gln Gly His Gly Thr His Val Ala Gly Ser Ala Leu Ala Asn
180 185 190

Gly Gly Thr Gly Ser Gly Val Tyr Gly Val Ala Pro Glu Ala Asp Leu
195 200 205

Trp Ala Tyr Lys Val Leu Gly Asp Asp Gly Ser Gly Tyr Ala Asp Asp
210 215 220

Ile Ala Glu Ala Ile Arg His Ala Gly Asp Gln Ala Thr Ala Leu Asn
225 230 235 240

Thr Lys Val Val Ile Asn Met Ser Leu Gly Ser Ser Gly Glu Ser Ser
245 250 255

Leu Ile Thr Asn Ala Val Asp Tyr Ala Tyr Asp Lys Gly Val Leu Ile
260 265 270

Ile Ala Ala Ala Gly Asn Ser Gly Pro Lys Pro Gly Ser Ile Gly Tyr
275 280 285

Pro Gly Ala Leu Val Asn Ala Val Ala Val Ala Leu Glu Asn Thr
290 295 300

Ile Gln Asn Gly Thr Tyr Arg Val Ala Asp Phe Ser Ser Arg Gly His
305 310 315 320

Lys Arg Thr Ala Gly Asp Tyr Val Ile Gln Lys Gly Asp Val Glu Ile
325 330 335

Ser Ala Pro Gly Ala Ala Val Tyr Ser Thr Trp Phe Asp Gly Gly Tyr
340 345 350

Ala Thr Ile Ser Gly Thr Ser Met Ala Ser Pro His Ala Ala Gly Leu
355 360 365

Ala Ala Lys Ile Trp Ala Gln Ser Pro Ala Ala Ser Asn Val Asp Val
370 375 380

Arg Gly Glu Leu Gln Thr Arg Ala Ser Val Asn Asp Ile Leu Ser Gly
385 390 395 400

Asn Ser Ala Gly Ser Gly Asp Asp Ile Ala Ser Gly Phe Gly Phe Ala
405 410 415

Lys Val Gln

<210> 4
<211> 310
<212> PRT
<213> B. sphaericus sphericase

<220>
<221> PEPTIDE
<222> (1)..(310)

<400> 4

Arg Ala Ser Gln Gln Ile Pro Trp Gly Ile Lys Ala Ile Tyr Asn Asn
1 5 10 15

Asp Thr Leu Thr Ser Thr Thr Gly Gly Ser Gly Ile Asn Ile Ala Val
20 25 30

Leu Asp Thr Gly Val Asn Thr Ser His Pro Asp Leu Val Asn Asn Val
35 40 45

Glu Gln Cys Lys Asp Phe Thr Gly Ala Thr Thr Pro Ile Asn Asn Ser
50 55 60

Cys Thr Asp Arg Asn Gly His Gly Thr His Val Ala Gly Thr Ala Leu
65 70 75 80

Ala Asp Gly Gly Ser Asp Gln Ala Gly Ile Tyr Gly Val Ala Pro Asp
85 90 95

Ala Asp Leu Trp Ala Tyr Lys Val Leu Leu Asp Ser Gly Ser Gly Tyr
100 105 110

Ser Asp Asp Ile Ala Ala Ala Ile Arg His Ala Ala Asp Gln Ala Thr
115 120 125

Ala Thr Gly Thr Lys Thr Ile Ile Ser Met Ser Leu Gly Ser Ser Ala
130 135 140

Asn Asn Ser Leu Ile Ser Ser Ala Val Asn Tyr Ala Tyr Ser Lys Gly
145 150 155 160

Val Leu Ile Val Ala Ala Ala Gly Asn Ser Gly Tyr Ser Gln Gly Thr
165 170 175

Ile Gly Tyr Pro Gly Ala Leu Pro Asn Ala Ile Ala Val Ala Ala Leu
180 185 190

Glu Asn Val Gln Gln Asn Gly Thr Tyr Arg Val Ala Asp Tyr Ser Ser
195 200 205

Arg Gly Tyr Ile Ser Thr Ala Gly Asp Tyr Val Ile Gln Glu Gly Asp
210 215 220

Ile Glu Ile Ser Ala Pro Gly Ser Ser Val Tyr Ser Thr Trp Tyr Asn
225 230 235 240

Gly Gly Tyr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His Val
245 250 255

Ser Gly Leu Ala Ala Lys Ile Trp Ala Glu Asn Pro Ser Leu Ser Asn
260 265 270

Thr Gln Leu Arg Ser Asn Leu Gln Glu Arg Ala Lys Ser Val Asp Ile
275 280 285

Lys Gly Gly Tyr Gly Ala Ala Ile Gly Asp Asp Tyr Ala Ser Gly Phe
290 295 300

Gly Phe Ala Arg Val Gln
305 310

<210> 5
<211> 275
<212> PRT
<213> Bacillus amyloliquefaciens

<220>
<221> PEPTIDE
<222> (1)..(275)
<223> BPN'

<400> 5

Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
1 5 10 15

His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
20 25 30

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
35 40 45

Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
50 55 60

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
65 70 75 80

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
85 90 95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
100 105 110

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
115 120 125

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
130 135 140

Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
145 150 155 160

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
165 170 175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
180 185 190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
195 200 205

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
225 230 235 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
245 250 255

Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
260 265 270

Ala Ala Gln
275

<210> 6
<211> 269
<212> PRT
<213> *Bacillus lentinus*

<220>
<221> PEPTIDE
<222> (1)..(269)
<223> Savinase

<400> 6

Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
1 5 10 15

His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
20 25 30

Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
35 40 45

Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
50 55 60

His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
65 70 75 80

Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
85 90 95

Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
100 105 110

Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
115 120 125

Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
130 135 140

Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
145 150 155 160

Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
165 170 175

Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
180 185 190

Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
195 200 205

Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
210 215 220

Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
225 230 235 240

Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
245 250 255

Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
260 265

<210> 7
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(60)
<223> primer 28-35-CN

<400> 7
tagatctgga tgagtggawv yccctgtatc gaggacagcw rbttttacac cagaacctgt 60

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

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<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(18)
<223> primer 28-35-NC

<400> 8
tccactcatc cagatcta                                18

<210> 9
<211> 45
<212> DNA
<213> artificial

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(45)
<223> primer 71-72-73-CN (I)

<400> 9
aatcgaattg tttaaagcag cwvyygwccc ggccacatgc gtgcc      45

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(45)
<223> primer 71-72-73-CN (II)

<400> 10
aatcgaattg tttaaagcaa gwvyygwccc ggccacatgc gtgcc      45

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

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<220>
<221> misc_feature
<222> (1)..(45)
<223> primer 71-72-73-CN (III)

<400> 11
aatcgaattg tttaaagcgc cwvyygwccc gccacatgc gtgcc          45

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(18)
<223> primer 71-72-73-NC

<400> 12
gctttaaca attcgatt                                18

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(24)
<223> primer 139

<400> 13
gattaacgcg ttgccgcttc tgcg                         24

<210> 14
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(39)

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<223> primer 175-CN (I)

<400> 14
atcagtagct ccgactgcc a tgcgttcgc atagcg cgc 39

<210> 15
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(39)
<223> primer 175-CN (II)

<400> 15
atcagtagct ccgactgcc ctgcgttcgc atagcg cgc 39

<210> 16
<211> 18
<212> DNA
<213> artificial

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(18)
<223> primer 175-NC

<400> 16
gcagtccgag ctactgat 18

<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(39)
<223> primer 224-CN

<400> 17

cgcacctgca acatgaggcg hagccatcga tgtaccgtt	39
<210> 18	
<211> 18	
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<213> Artificial Sequence	
<220>	
<223> synthetic oligopeptide	
<220>	
<221> misc_feature	
<222> (1)..(18)	
<223> primer 224-NC	
<400> 18	
cctcatgttg caggtgcg	18
<210> 19	
<211> 22	
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<223> synthetic oligopeptide	
<220>	
<221> misc_feature	
<222> (1)..(22)	
<223> primer 317-CN	
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tggcgcaatc ggtaccatgg gg	22
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<213> TY145 subtilase DNA	
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gcggtagccaa gtacacaaac cccttggggc ataaagtcaa tttataatga tcaatcaatt	60
acaaaaaacaa ctggaggcag cgaaattaag gtagctgttt tagatacagg ggtttataaca	120
agccatttag attagctgg ttctgccag caatgcaagg attttaccca atctaattcct	180
tttagtagatg gttcatgcac cgatcgccaa gggcatggta cacatgttgc cggaactgta	240
ttggcgcatg gaggcagtaa tggacaaggc gtttacgggg tggctccgca agcgaaacta	300
tgggcataa aagtattagg agataacggc agcggatact ctgatgatat tgcagcagct	360

atcagacatg tagctgatga agcttcacgt acaggttcca aagtagtaat taatatgtcg	420
ctaggttcat ctgccaagga ttcattgatt gctagtgcag tagattatgc atatggaaaa	480
ggtgtattaa tcgttgctgc ggctggtaat agtgggtcag gcagcaatac aatccgctt	540
cctggcgggc ttgtaaatgc agtggcagta gcgcattgg agaatgttca gcaaaatgga	600
acttatcgag tagctgattt ctcatctaga gggaaatccgg caactgctgg agattatac	660
attcaagagc gtgatattga agtttcagct ccgggagcaa gtgtagagtc tacatggtac	720
actggcggtt ataatacgat cagcggtaca tcaatggcta cacctcatgt agctgggtta	780
gctgctaaaa tctggtcagc gaataacttca ttaagtcata gccaaactgcg cacagaattg	840
caaaaatcgcg ctaaagtata tgatattaaa ggtggtatcg gagccggaac aggtgacgat	900
tatgcatcag ggttcggata tccaagagta aaataa	936

<210> 21
 <211> 1143
 <212> DNA
 <213> *Bacillus latus, Savinase*

<400> 21	
atgaagaaac cgttgggaa aattgtcgca agcacccgac tactcatttc tggtgtttt	60
agttcatcga tcgcattcggc tgctgaagaa gcaaaagaaa aatatttaat tggcttaat	120
gagcaggaag ctgtcagtga gttttagaa caagtagagg caaatgacga ggtcgccatt	180
ctctctgagg aagaggaagt cggaaattgaa ttgcttcatg aatttgaac gattcctgtt	240
ttatccgtt agttaagccc agaagatgtg gacgcgttg aactcgatcc agcgattct	300
tatattgaag aggatgcaga agtaacgaca atggcgcaat cggtaccatg ggaaattagc	360
cgtgtgcaag ccccgactgc ccataaccgt ggattgacag gttctgggtaaaagttgt	420
gtcctcgata cagggatatac cactcatcca gatctaaata ttctgggtgg cgcaagctt	480
gtaccagggg aaccgtcgac tcaagatgg aatgggcattgc acacgcattgt ggccggacg	540
atcgctgtt taaacaattt gattggcggtt ctggcgtag cgccgagcgc tgagctatac	600
gctgttaaag tccttaggggc gagcgggtca gggtcggtca gctcgattgc ccaaggattt	660
gaatggcag ggaacaatgg catgcacgtt gctaatttga gtttaggaag cccttcgcca	720
agtgccacac tcgagcaagc tgttaatagc gcgacttcta gaggcggtct tggtgtacg	780
gcatctggaa attcagggtgc aggctcaatc agctatccgg cgccgtatgc gaacgcattg	840
gcagtcggag ctactgatca aaacaacaac cgcgctagct tttcacagta tggcgagggc	900

cttgacattg tcgcacccgg ggttaaacgtg cagagcacat acccaggttc aacatatgcc	960
agcttaaacg gtacatcgat ggctactcct catgttgcag gtgcggccgc ccttgttaaa	1020
caaaaagaacc catcttggtc taatgtacaa attcgaaatc atctaaagaa tacggcaact	1080
agttaggaa gcacgaactt gtatgaaagc ggacttgtt aacgcagaagc ggcaacgcgt	1140
taa	1143

<210> 22
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 22

Ser Ala Lys Asp Ser Leu Ile Ala Ser Ala Val Asp		
1	5	10

<210> 23
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 23

Pro Ser Pro Ser Ala Thr Leu Glu Gln Ala Val Asn		
1	5	10

<210> 24
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 24

Ala Gly Asn Ser Gly Ser Gly Asn Thr Ile Gly Phe Pro Gly Gly			
1	5	10	15

Leu Val

<210> 25
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 25

Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr Pro Ala Arg Tyr Ala
1 5 10 15

<210> 26
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 26

Ala Ser Val Glu Ser Thr Trp Tyr Thr Gly Gly Tyr Asn Thr Ile Ser
1 5 10 15

<210> 27
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 27

Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala Ser Leu Asn
1 5 10 15

<210> 28
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 28

Met Ser Leu Gly Ser Ser Gly
1 5

<210> 29

<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 29

Leu Ser Leu Gly Ser Pro Ser
1 5

<210> 30
<211> 12
<212> PRT
<213> Artificial sequence

<220>
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<400> 30

Met Ser Leu Gly Ser Ser Gly Glu Ser Ser Leu Ile
1 5 10

<210> 31
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 31

Leu Ser Leu Gly Ser Pro Ser Pro Ser Ala Thr Leu
1 5 10

<210> 32
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 32

Asn Asn Ser Ser Ile Thr Gln Thr
1 5

<210> 33
<211> 8

<212> PRT
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<220>
<223> Highly mobile region of Savinase

<400> 33

Val Gln Ala Pro Ala Ala His Asn
1 5

<210> 34
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 34

Thr Val Gly Thr Thr Tyr Thr Asn
1 5

<210> 35
<211> 7
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<220>
<223> Highly mobile region of Savinase

<400> 35

Val Pro Gly Glu Pro Ser Thr
1 5

<210> 36
<211> 7
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<220>
<223> Highly mobile region of Savinase

<400> 36

Ser Gly Glu Ser Ser Leu Ile
1 5

<210> 37
<211> 7
<212> PRT

<213> Artificial sequence

<220>

<223> Highly mobile region of Savinase

<400> 37

Pro Ser Pro Ser Ala Thr Leu

1 5

<210> 38

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Highly mobile region of Savinase

<400> 38

Trp Phe Asp Gly Gly Tyr Ala Thr Ile

1 5

<210> 39

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Highly mobile region of Savinase

<400> 39

Tyr Pro Gly Ser Thr Tyr Ala Ser Leu

1 5

<210> 40

<211> 8

<212> PRT

<213> Artificial sequence

<220>

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<400> 40

Thr Val Gly Thr Asn Phe Thr Asp

1 5

<210> 41

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<212> PRT

<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 41

Val Pro Gly Glu Pro Ser Thr
1 5

<210> 42
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<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 42

Asn Gly Gly Thr Gly Ser
1 5

<210> 43
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 43

Ala Leu Asn Asn Ser Ile
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Highly mobile region of Savinase

<400> 44

Asp Asp Gly Ser Gly Tyr Ala
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